

Sequence alignment of NRBP2 and NRBP1 across various species. The alignment shows conservation of amino acid residues across the entire protein length. The top sequence is NRBP2.h, followed by NRBP1.h, and then other species. Colored boxes highlight conserved regions, primarily in the N-terminal domain.

NRBP2.h
34866843.m
22219434.m
NRBP1.h
24644388.f
31224689.i
17507967.w
15835040.b
15604864.b
19173602.y
1.m